SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Deisher, Theresa A.
                Conklin, Darrell C.
                Raymond, Fenella
                Bukowski, Thomas R.
                Holderman, Susan D.
                Hansen, Birgit
                Sheppard, Paul O.

(ii) TITLE OF THE INVENTION: NOVEL FGF HOMOLOGS

(iii) NUMBER OF SEQUENCES: 20

(iv) CORRESPONDENCE ADDRESS:
   (A) ADDRESSEE: ZymoGenetics, Inc.
   (B) STREET: 1201 Eastlake Avenue East
   (C) CITY: Seattle
   (D) STATE: WA
   (E) COUNTRY: USA
   (F) ZIP: 98102

(v) COMPUTER READABLE FORM:
   (A) MEDIUM TYPE: Diskette
   (B) COMPUTER: IBM Compatible
   (C) OPERATING SYSTEM: DOS
   (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:
   (A) APPLICATION NUMBER:
   (B) FILING DATE:
   (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
   (A) APPLICATION NUMBER:
   (B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Sawislak, Deborah A
(B) REGISTRATION NUMBER: 37,438
(C) REFERENCE/DOCKET NUMBER: 96-20

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 206-442-6672
(B) TELEFAX: 206-442-6678
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 917 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 1...621
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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ATG TAT TCA GCG CCC TCC GCC TGC ACT TGC CTG TGT TTA CAC TTC CTG        48
Met Tyr Ser Ala Pro Ser Ala Cys Thr Cys Leu Cys Leu His Phe Leu
1               5                   10              -   15

CTG CTG TGC TTC CAG GTA CAG GTG CTG GTT GCC GAG GAG AAC GTG GAC        96
Leu Leu Cys Phe Gln Val Gln Val Leu Val Ala Glu Glu Asn Val Asp
                20                  25              30

TTC CGC ATC CAC GTG GAG AAC CAG ACG CGG GCT CGG GAC GAT GTG AGC       144
Phe Arg Ile His Val Glu Asn Gln Thr Arg Ala Arg Asp Asp Val Ser
                35                  40              45

CGT AAG CAG CTG CGG CTG TAC CAG CTC TAC AGC CGG ACC AGT GGG AAA       192
Arg Lys Gln Leu Arg Leu Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys
        50                  55                  60
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CAC ATC CAG GTC CTG GGC CGC AGG ATC AGT GCC CGC GGC GAG GAT GGG      240
His Ile Gln Val Leu Gly Arg Arg Ile Ser Ala Arg Gly Glu Asp Gly
65                  70                  75                  80

GAC AAG TAT GCC CAG CTC CTA GTG GAG ACA GAC ACC TTC GGT AGT CAA      288
Asp Lys Tyr Ala Gln Leu Leu Val Glu Thr Asp Thr Phe Gly Ser Gln
                85                  90                  95

GTC CGG ATC AAG GGC AAG GAG ACG GAA TTC TAC CTG TGC ATG AAC CGC      336
Val Arg Ile Lys Gly Lys Glu Thr Glu Phe Tyr Leu Cys Met Asn Arg
                100                 105                 110

AAA GGC AAG CTC GTG GGG AAG CCC GAT GGC ACC AGC AAG GAG TGT GTG      384
Lys Gly Lys Leu Val Gly Lys Pro Asp Gly Thr Ser Lys Glu Cys Val
                115                 120                 125

TTC ATC GAG AAG GTT CTG GAG AAC AAC TAC ACG GCC CTG ATG TCG GCT      432
Phe Ile Glu Lys Val Leu Glu Asn Asn Tyr Thr Ala Leu Met Ser Ala
    130                 135                 140

AAG TAC TCC GGC TGG TAC GTG GGC TTC ACC AAG AAG GGG CGG CCG CGG      480
Lys Tyr Ser Gly Trp Tyr Val Gly Phe Thr Lys Lys Gly Arg Pro Arg
145                 150                 155                 160

AAG GGC CCC AAG ACC CGG GAG AAC CAG CAG GAC GTG CAT TTC ATG AAG      528
Lys Gly Pro Lys Thr Arg Glu Asn Gln Gln Asp Val His Phe Met Lys
                165                 170                 175

CGC TAC CCC AAG GGG CAG CCG GAG CTT CAG AAG CCC TTC AAG TAC ACG      576
Arg Tyr Pro Lys Gly Gln Pro Glu Leu Gln Lys Pro Phe Lys Tyr Thr
                180                 185                 190

ACG GTG ACC AAG AGG TCC CGT CGG ATC CGG CCC ACA CAC CCT GCC TAGGC  626
Thr Val Thr Lys Arg Ser Arg Arg Ile Arg Pro Thr His Pro Ala
                195                 200                 205

CACCCCGCCG CGGCCCTCAG GTCGCCCTGG CCACACTCAC ACTCCCAGAA AACTGCATCA    686
GAGGAATATT TTTACATGAA AAATAAGGAT TTTATTGTTG ACTTGAAACC CCCGATGACA    746
AAAGACTCAC GCAAAGGGAC TGTAGTCAAC CCACAGGTGC TTGTCTCTCT CTAGGAACAG    806
ACAACTCTAA ACTCGTCCCC AGAGGAGGAC TTGAATGAGG AAACCAACAC TTTGAGAAAC    866
CAAAGTCCTT TTTCCCAAAG GTTCTGAAAA AAAAAAAAAA AAAAACTCGA G            917
```

(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 207 amino acids
       (B) TYPE: amino acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein
    (v) FRAGMENT TYPE: internal

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Tyr Ser Ala Pro Ser Ala Cys Thr Cys Leu Cys Leu His Phe Leu
1               5               10              15
Leu Leu Cys Phe Gln Val Gln Val Leu Val Ala Glu Glu Asn Val Asp
            20              25              30
Phe Arg Ile His Val Glu Asn Gln Thr Arg Ala Arg Asp Asp Val Ser
        35              40              45
Arg Lys Gln Leu Arg Leu Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys
    50              55              60
His Ile Gln Val Leu Gly Arg Arg Ile Ser Ala Arg Gly Glu Asp Gly
65                  70              75              80
Asp Lys Tyr Ala Gln Leu Leu Val Glu Thr Asp Thr Phe Gly Ser Gln
            85              90              95
Val Arg Ile Lys Gly Lys Glu Thr Glu Phe Tyr Leu Cys Met Asn Arg
            100             105             110
Lys Gly Lys Leu Val Gly Lys Pro Asp Gly Thr Ser Lys Glu Cys Val
            115             120             125
Phe Ile Glu Lys Val Leu Glu Asn Asn Tyr Thr Ala Leu Met Ser Ala
    130             135             140
Lys Tyr Ser Gly Trp Tyr Val Gly Phe Thr Lys Lys Gly Arg Pro Arg
145             150             155             160
Lys Gly Pro Lys Thr Arg Glu Asn Gln Gln Asp Val His Phe Met Lys
            165             170             175
Arg Tyr Pro Lys Gly Gln Pro Glu Leu Gln Lys Pro Phe Lys Tyr Thr
            180             185             190
Thr Val Thr Lys Arg Ser Arg Arg Ile Arg Pro Thr His Pro Ala
        195             200             205

        (2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 24 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single

   (D) TOPOLOGY: linear

 (vii) IMMEDIATE SOURCE:
    (B) CLONE: ZC11676

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGACTTGACT ACCGAAGGTG TCTG                                24

     (2) INFORMATION FOR SEQ ID NO:4:

 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 23 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

 (vii) IMMEDIATE SOURCE:
    (B) CLONE: ZC11677

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTCGATGTGA GCCGTAAGCA GCT                                23

     (2) INFORMATION FOR SEQ ID NO:5:

 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 26 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

 (vii) IMMEDIATE SOURCE:
    (B) CLONE: ZC12053

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCATACTTGT CCCCATCCTC GCCGCG                             26

     (2) INFORMATION FOR SEQ ID NO:6:

 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 621 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single

        (D) TOPOLOGY: linear


        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGTAYWSNG CNCCNWSNGC NTGYACNTGY YTNTGYYTNC AYTTYYTNYT NYTNTGYTTY    60
CARGTNCARG TNYTNGTNGC NGARGARAAY GTNGAYTTYM GNATHGAYGT NGARAARCAR   120
ACNMGNGCNM GNGAYGAYGT NWSNMGNAAR CARYTNMGNY TNTAYCARYT NTAYWSNMGN   180
ACNWSNGGNA ARCAYATHCA RGTNYTNGGN MGNMGNATHW SNGCNMGNGG NGARGAYGGN   240
GAYAARTAYG CNCARYTNYT NGTNGARACN GAYACNTTYG GNWSNCARGT NMGNATHAAR   300
GGNAARGARA CNGARTTYTA YYTNTGYATG AAYMGNAARG GNAARYTNGT NGGNAARCCN   360
GAYGGNACNW SNAARGARTG YGTNTTYATH GARAARGTNY TNGARAAYAA YTAYACNGCN   420
YTNATGWSNG CNAARTAYWS NGGNTGGTAY GTNGGNTTYA CNAARAARGG NMGNCCNMGN   480
AARGGNCCNA ARACNMGNGA RAAYCARCAR GAYGTNCAYT TYATGAARMG NTAYCCNAAR   540
GGNCARCCNG ARYTNCARAA RCCNTTYAAR TAYACNACNG TNACNAARMG NWSNMGNMGN   600
ATHMGNCCNA CNCAYCCNGC N                                            621

        (2) INFORMATION FOR SEQ ID NO:7:


    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 47 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (vii) IMMEDIATE SOURCE:
        (B) CLONE: ZC12652

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TATTTATCTA GACTGGTTCC GCGTGCCGCC GAGGAGAACG TGGACTT                 47

        (2) INFORMATION FOR SEQ ID NO:8:


    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 33 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (vii) IMMEDIATE SOURCE:
        (B) CLONE: ZC12631

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTATTTGTCG ACTCAGGCAG GGTGTGTGGG CCG 33

    (2) INFORMATION FOR SEQ ID NO:9:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 22 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (vii) IMMEDIATE SOURCE:
      (B) CLONE: ZC15290

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCCGAGGAGA ACGTGGACTT CC 22

    (2) INFORMATION FOR SEQ ID NO:10:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 47 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (vii) IMMEDIATE SOURCE:
      (B) CLONE: ZC15270

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TATTTATCTA GAGATGACGA TGACAAGGCC GAGGAGAACG TGGACTT 47

    (2) INFORMATION FOR SEQ ID NO:11:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 41 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (vii) IMMEDIATE SOURCE:
      (B) CLONE: ZC13497

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGCATTGCTA AAGAAGAAGG TGTAAGCTTG GACAAGAGAG A                    41

      (2) INFORMATION FOR SEQ ID NO:12:

     (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 63 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

     (vii) IMMEDIATE SOURCE:
      (B) CLONE: ZC15131

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGTGTAAGCT TGGACAAGAG AGAGGAGAAC GTGGACTTCC GCATCCACGT GGAGAACCAG    60
ACG                                                                63

      (2) INFORMATION FOR SEQ ID NO:13:

     (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 39 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

     (vii) IMMEDIATE SOURCE:
      (B) CLONE: ZC15134

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCGGCTGTAG AGCTGGTACA GCCGCAGCTG CTTACGGCT                          39

      (2) INFORMATION FOR SEQ ID NO:14:

     (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 42 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

     (vii) IMMEDIATE SOURCE:
      (B) CLONE: ZC13529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTTCAGAAGC CCTTCAAGTA CACGACGGTG ACCAAGAGGT CC          42

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 61 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
   (B) CLONE: ZC13525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ACGACGGTGA CCAAGAGGTC CCGTCGGATC CGGCCCACAC ACCCTGCCTA GGGGGAATTC          60
G          61

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 61 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
   (B) CLONE: ZC13526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CAAACAGGCA GCCCTAGAAT ACTAGTGTCG ACTCGAGGAT CCGAATTCCC CCTAGGCAGG          60
G          61

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 44 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(vii) IMMEDIATE SOURCE:
   (B) CLONE: ZC13528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CTCAAAAATT ATAAAAATAT CCAAACAGGC AGCCCTAGAA TACT                    44

   (2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 62 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
   (B) CLONE: ZC15132


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CAGCCGCAGC TGCTTAGCGC TCACATCGTC CCGAGCCCGC GTCTGGTTCT CCACGTGGAT GC    62


   (2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 141 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: double
   (D) TOPOLOGY: linear


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AGCATTGCTG CTAAAGAAGA AGGTGTAAGC TTGGACAAGA GAGAGGAGAA CGTGGACTTC    60
CGCATCCACG TGGAGAACCA GACGCGGGCT CGGGACGATG TGAGCCGTAA GCAGCTGCGG   120
CTGTACCAGC TCTACAGCCG G                                            141

   (2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 144 base pairs
   (B) TYPE: nucleic acid

      (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear


     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```
CTTCAGAAGC CCTTCAAGTA CACGACGGTG ACCAAGAGGT CCCGTCGGAT CCGGCCCACA      60
CACCCTGCCT AGGGGGAATT CGGATCCTCG AGTCGACACT AGTATTCTAG GGCTGCCTGT     120
TTGGATATTT TTATAATTTT TGAG                                            144
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